

N. Basi

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/051,843

DATE: 01/14/1999
TIME: 15:51:49

Input Set: I051843.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

new format

1 <110> APPLICANT: Willson, Tracy
2 Nicola, Nicos A.
3 Hilton, Douglas J.
4 Metcalf, Donald
5 Zhang, Jian G.
6 <120> TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
7 ENCODING SAME
8 <130> FILE REFERENCE: Davies cc
9 <140> CURRENT APPLICATION NUMBER: US/09/051,843
10 <141> CURRENT FILING DATE: 1998-06-29
11 <160> NUMBER OF SEQ ID NOS: 8
12 <170> SOFTWARE: PatentIn Ver. 2.0
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44 region

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53 Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
54 1 5 10 15
W--> 55 acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca 156
56 Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
57 20 25 30
58 cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata 204
59 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
60 35 40 45
61 tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga 252
62 Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
63 50 55 60
64 tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa 300
65 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
66 65 70 75 80
67 act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag 348
68 Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
69 85 90 95
70 gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg 396
71 Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
72 100 105 110
73 gtg aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg 444
74 Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
75 115 120 125
76 act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc 492
77 Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
78 130 135 140
79 tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac 540
80 Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
81 145 150 155 160
82 tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat 588
83 Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
84 165 170 175
85 aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa 636
86 Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
87 180 185 190
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90 195 200 205
91 gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat 732
92 Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
93 210 215 220
94 gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt 780

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100     tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat      876
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103     att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga      924
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106     aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac      972
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109     gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt      1020
110     Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
111     305                                310                                315                                320
112     gat gac aac aaa ctg tgg agt gat tgg agt gaa gca cag agt ata ggt      1068
113     Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
114     325                                330                                335
115     aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca      1116
116     Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
117     340                                345                                350
118     gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg      1164
119     Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
120     355                                360                                365
121     ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt      1212
122     Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
123     370                                375                                380
124     aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag      1260
125     Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
126     385                                390                                395                                400
127     tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg      1308
128     Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
129     405                                410                                415
130     ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc      1358
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154 50 55 60
155 Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
156 65 70 75 80
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158 85 90 95
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160 100 105 110
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162 115 120 125
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168 165 170 175
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W--> 171 Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
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174 210 215 220
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176 225 230 235 240
177 Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
178 245 250 255
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180 260 265 270
181 Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
182 275 280 285
183 Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
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188 325 330 335
189 Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
190 340 345 350
191 Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
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193 Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
194 370 375 380

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211      Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
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214      Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
215                      20                      25                      30
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219      tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252
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224                      65                      70                      75                      80
225      act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348
226      Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
227                      85                      90                      95
228      gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396
229      Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
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231      gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg 444
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233                      115                      120                      125
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236                      130                      135                      140
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238      Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
239                      145                      150                      155                      160
240      tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt 588
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242                      165                      170                      175
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Input Set: I051843.RAW

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